

1. Specimens: Homo Sapiens (MN)
 2. Date: 14-May-1998
 3. Location: New York
 4. Change: 24-Sep-1998
 5. User: [redacted]


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      : : : : : : : : : :
Db 652 EGILTEGDAVGSKNLFVEFSALT 676

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RESULT 14

amidase Methanobacterium thermoautotrophicum (strain Delta H)
C.Species: Methanobacterium thermoautotrophicum
C.Date: 01/01/1977
C.Accession: D59006
P.Strain: 167 Thermophilic Strain 167 (Enrichment) from H. Embolsky, T. Althage, T. G. Q. G. S. Chaudhry, R. M. Vignales, R. Wang, Y. W. K. Chow, K. J. Gibson, R. J. Wainwright, N. J. Bacteriol. 179, 7135-7155, 1997
J.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H (strain 167) (Complete genome sequence of Methanobacterium thermoautotrophicum Delta H (strain 167))
A.Reference number: A69000; M01D:9807514
A.Accession: D59006
A.Strain: Preliminary host for acid-requirement studies
A.Molecule type: DNA
A.Residues: 1454 <MTH>
A.Coverage: 100% (100% coverage) (100% coverage) (100% coverage) (100% coverage) (100% coverage)
A.Experimental source: strain Delta H
C.Chemicals:
A.Gene: MTH1496
A.Start codon: GTG
C.Importantly: Indoleacetylamine hydrolase

Query Match	32.0%	Score 43.51	DB 2	Length 454
Best Local Similarity	26.3%	Prod. No. 32		
Matches	7	Conservative	12	Mismatches 6, Indels 5, Gaps 1

2 DIGIT 110MTCF-...-PKHLLVDFLOSIS 26

Db 284 EGAEVELDFGYIDLCPTYYLINVEFFS 313

RESULT 15

Cleavage and polypeptide isolation specificity factor 100k chain - bovine
 N/Atername names: GPCSF_100K_chain
 C/Species: Bos primigenius taurus (cattle)
 C/Dat: 03-Sep-1997 #E01686=proteinase 03-Sep-1997 #E01686=range 10-Sep-1997
 C/Accession: A56351
 R/Jenny: A.; Hauri, H.P.; Keller, W.
 M/I Cell: Biol. 14, 8183-8190, 1994
 A>Title: Characterization of cleavage and polypeptidation specificity factor and cloning
 A/Reference number: A56351; MIMD196059047
 A/Accession: A56351
 A>Status: preliminary; nucleio acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1782 <FE>
 A/Cross-references: GR:X75931; NID:9450037; PID:94599683
 A>Note: parts of this sequ-ence were confirmed by peptide sequencing

Every Match	(2.78)	Score 43.5;	DB 2;	Length 782;
Best Local Similarity	34.58;	Pred. No. 58;		
Matches	10, Conserved	5, Mismatches	7; Indels	7; Gaps
				1

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QY 4 CLLIQ-----MDFGFPKHLVDLQSL 25

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20 CYLLVBERKLLDJSWDEHFSMDITSL 48

Search completed: January 21, 2000, 19:22:14
Job time: 553 sec

